

FIG. 1

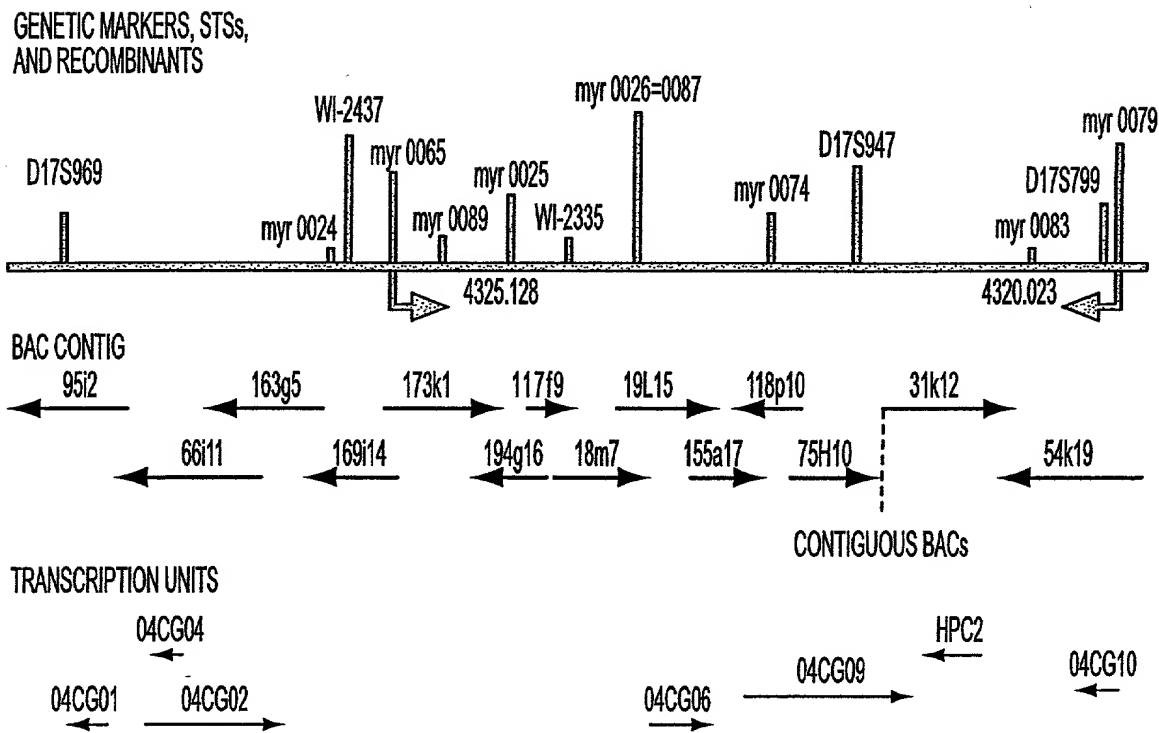


FIG. 2A

BAC 31k12 WITH 2 EXONS OF 04CG09 AND THE HPC2 TRANSCRIPTION UNIT

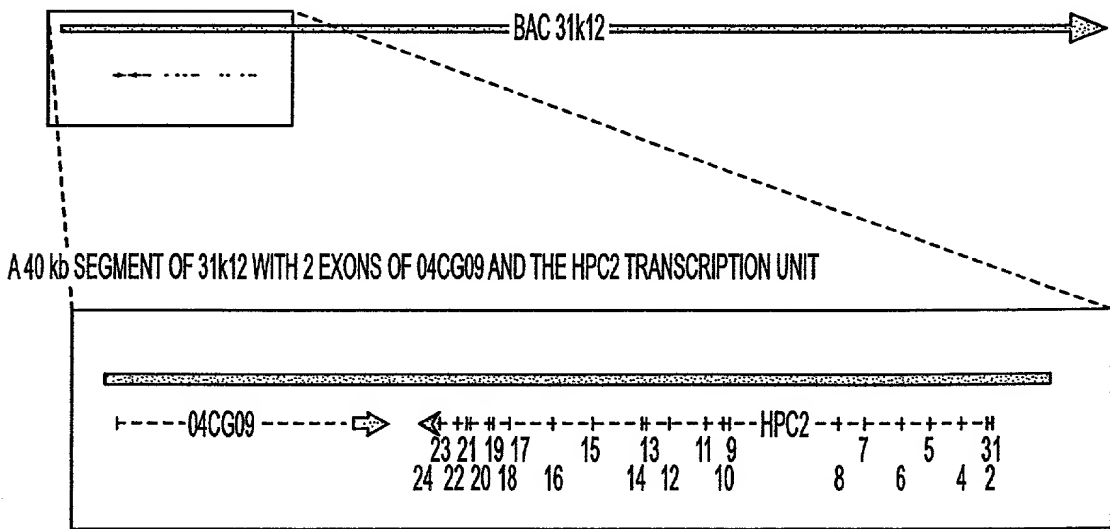


FIG. 2B



Hs.HPC2.exon1	cgcgggcgtaggtgaccggcggtttctcagttttggtggagacggggcg
Hs.HPC2.exon1.pep	
Mm.HPC2.exon2	tggcgggcgtagggggtctgggtgccttgtcagcctggtgtggtcgggtgc
Mm.HPC2.exon1.pep	----- ----- ----- ----- -----
	1 11 21 31 41
Hs.HPC2.exon1	ATGTGGGCGCTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACCATGTC
Hs.HPC2.exon1.pep	M--W--A--L--C--S--L--L--R--S--A--A--G--R--T--M--S--
Mm.HPC2.exon2	ATGTGGGCGCTCCGCTCACTGTTGCGTCCCTTGGCCTGCGCACCATGTC
Mm.HPC2.exon1.pep	M--W--A--L--R--S--L--L--R--P--L--G--L--R--T--M--S--
	----- ----- ----- ----- -----
	51 61 71 81 91
Hs.HPC2.exon1	GCAGGGACGCACCATATCGCAGGCACCCGCCCGCGAGCGGCCGCGCA
Hs.HPC2.exon1.pep	-Q--G--R--T--I--S--Q--A--P--A--R--R--E--R--P--R--K
Mm.HPC2.exon2	GCAGGGT-----TCGGCTCGTCGGCCGCGGCCACCCA
Mm.HPC2.exon1.pep	-Q--G-----S--A--R--R--P--R--P--P--K
	----- ----- ----- ----- -----
	101 111 121 131 141
Hs.HPC2.exon1	AGGACCCGCTGCGGCACCTGCGCACGCGAGAGAAGCGCGGACCGTCGGGG
Hs.HPC2.exon1.pep	--D--P--L--R--H--L--R--T--R--E--K--R--G--P--S--G--
Mm.HPC2.exon2	AAGACCCACTGCGACACCTGCGTACGCGGGAGAAGCGCGGCCCGGGT---
Mm.HPC2.exon1.pep	--D--P--L--R--H--L--R--T--R--E--K--R--G--P--G-----
	----- ----- ----- ----- -----
	151 161 171 181 191
Hs.HPC2.exon1	TGCTCCGGCGGCCCAAACACCGTGTACCTGCAGGTGGTGGCAGCGGGTAG
Hs.HPC2.exon1.pep	C--S--G--G--P--N--T--V--Y--L--Q--V--V--A--A--G--S--
Mm.HPC2.exon2	---CCCGGGGGCCCAACACCGTGTACCTGCAGGTGGTGGCGGGCGGGCGG
Mm.HPC2.exon1.pep	---P--G--G--P--N--T--V--Y--L--Q--V--V--A--A--G--G--
	----- ----- ----- ----- -----
	201 211 221 231 241
Hs.HPC2.exon1	CCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTCAACCGgtcag
Hs.HPC2.exon1.pep	-R--D--S--G--A--A--L--Y--V--F--S--E--F--N
Mm.HPC2.exon2	CCGGGACGCGGGGGCTGCTCTCTATGTCTTCTCGGAATACAACAGgtcag
Mm.HPC2.exon1.pep	-R--D--A--G--A--A--L--Y--V--F--S--E--Y--N
	----- ----- ----- ----- -----
	251 261 271 281 291
Hs.HPC2.exon1	tcaacgagccacgccccgtcccgtgggccctcagtgcggcgagcctct
Hs.HPC2.exon1.pep	
Mm.HPC2.exon2	agtgggcccagagccctgggggattggccccagcgccacgtgctcgggag
Mm.HPC2.exon1.pep	----- ----- ----- ----- -----
	301 311 321 331 341

FIG. 4

FIG. 5A

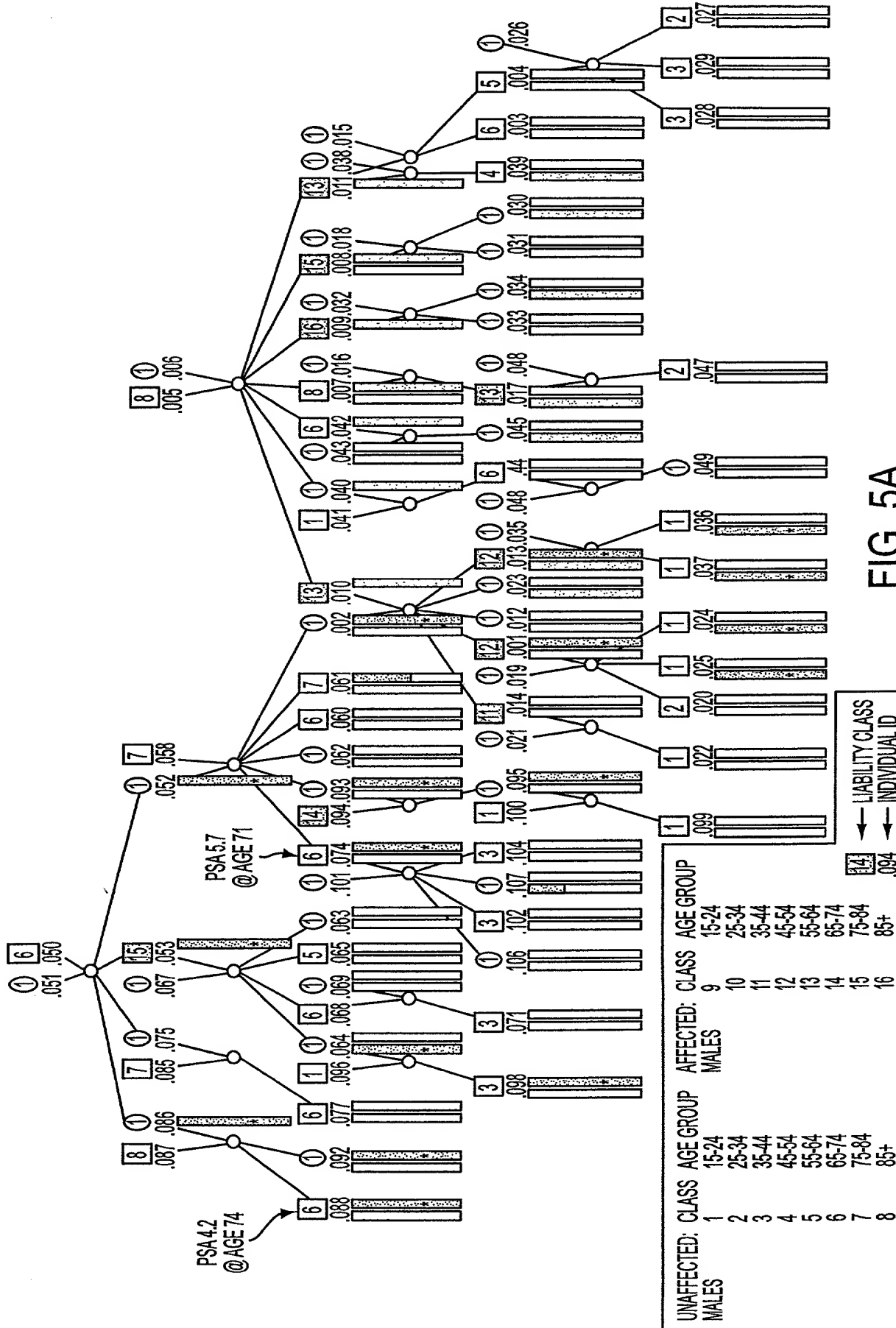


FIG. 5A

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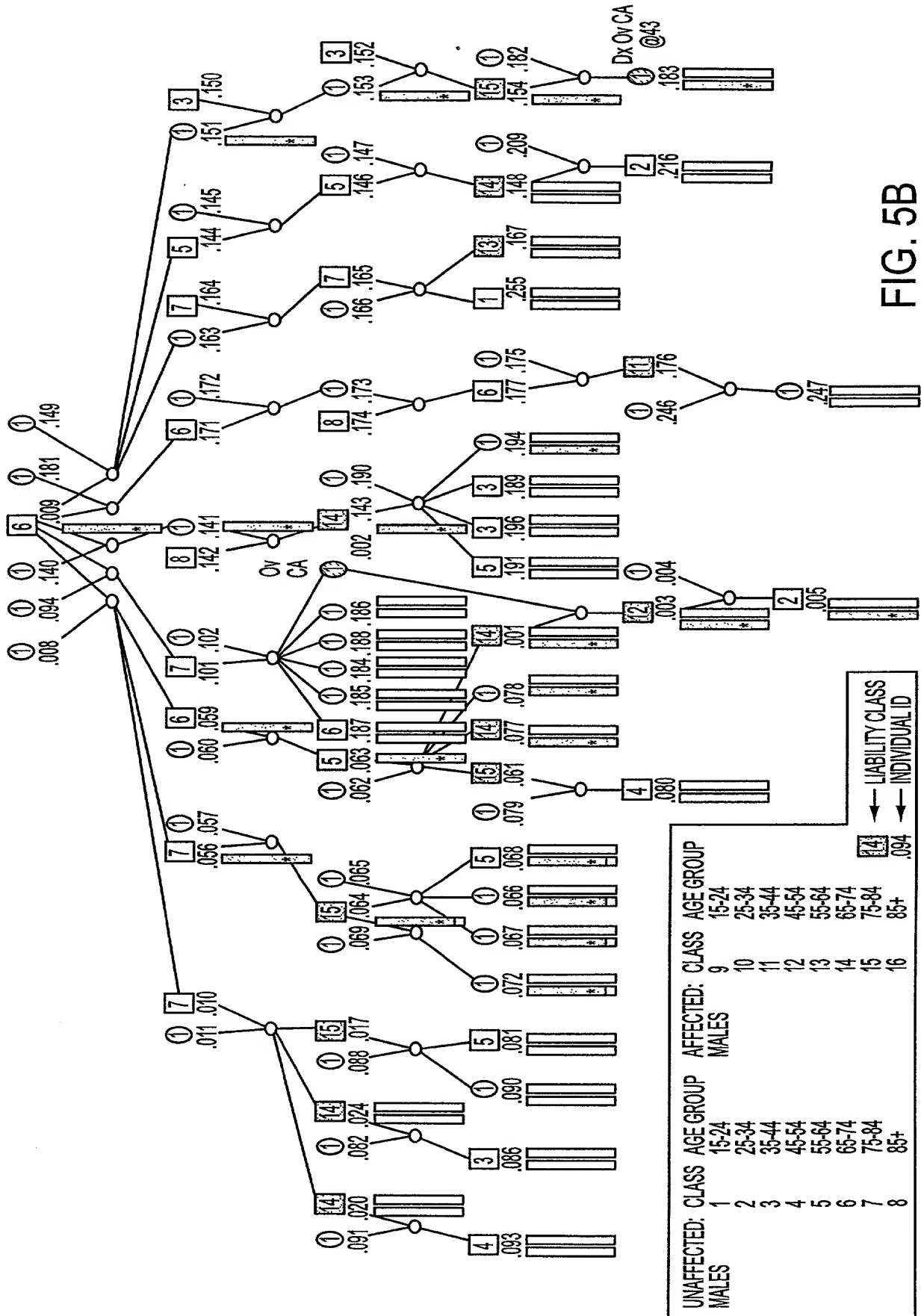


FIG. 5B

TABLE 2833660

(HSA) ELAC2	1	MWALCSLLRSAAAGTWSQRTISQAPARRRPRXDPPLHLTREKRGSGCGGENTVYLQVVA
(MMU) Elac2	1	MWALRSLRPLGLRTWSQ.....SARRPRSPKDPPLHLTREKRG.....GPGGNTVYLQVVA
(CEL) CE16965	1	MKNLFFGKIVSRHLISSTCSLFDNNNEELLESIKERTARNRRILQKSSSHLKAREYNASISNLRQMAAVQKKQAAHEPPANS·IVNIPSQVSTIEVLG
(ATH) gi6850339	1	MENNEATNGSKSSNSGFVNKRRAEGPDITDKKRNLERKSQK·LNPNTIAYAQILG
(SCE) YKR079C	1	MFTFIPTTH
(HSA) ELAC2	65	AGSRDGAALYWFSEYNR·YLFNCGEGVQRLMQEHLKVARNDNIFLT·RMHWSNVGGLSCMLTLTKETGLPK·CVLSGPPQLEKYL·EAIKIF.....
(MMU) Elac2	57	AGRDAGAALYWFSEYNR·YLFNCGEGVQRLMQEHLKVARNDNIFLT·RMHWSNVGGLSCMLTLTKETGLPK·CVLSGPPQLEKYL·EAIKIF.....
(CEL) CE16965	100	N·GTGLLRACFIILRTPKLT·YMFNCPENACRFLLWQLEIRSSVVDLFIIT·SANWDNITAGISSULLS·KEBNALS·TRLHGANNIKHFL·ECIRPFQDSD
(ATH) gi6850339	58	TGNDTQDTSSVLLFPDKQRFIFENAGEGLQRFCTEHIKILSKXIDHVFIS·RVCSETAGGLPCULLTLAGICEEGLSVNVWGPSDLNVLV·DAMKSFIPRA
(SCE) YKR079C	10	PTSDTKHPLLVSQAHGEKYFFFGKICGSGSORSLTENIRISKDKILFELGELNWSIDGGLPGMLTIADQCKSN·LVLHYGNDILNVIIVSTWRYVYVRF
(HSA) ELAC2	155SGPLK·GIELAVR.....PHSPEYEDETMTVYQPIHSEQRGKHQHQSPERPLSRLS·PERSDSESENEPHEL·P.....
(MMU) Elac2	147SGPLK·GIELAVR.....PHSPEYEDETMTVYQPIHSEQRGKHQHQSPERPLSRLS·PERSDSESENEPHEL·P.....
(CEL) CE16965	193YGSCKY·PSQVEER.....PYTMENYEDAGLKVITYP.....LSP·PLNIGSNNEKS.....
(ATH) gi6850339	156	ANVHTRSGPSPSTDPDVLVNDVVKISAI.....LKP·CHSEEDSCNKSGD.....
(SCE) YKR079C	108GIDLNDHMKDKVEYDKIIIAVKSFNKNGGEPRLGVFDSFGKGLRSIVA.....KMPFKHAPTRDYDPPSDPHLN.....
(HSA) ELAC2	226	..HGVSQRRGV·RDSLLVVAFLCKHLKRCNLFVLKAKEMGRVGTAAAPILAAVKDCKSIA·HEGREILAEELCTP.....PDPGAAPFWVECP·DESF
(MMU) Elac2	219	DSSAGANRKAWRDPSLVVAFVCKHLKRCNLFVLKAKELGLPVGTAAAPILAAVKDCKSIA·YEGREILAEELCTP.....PDPGLVFLWVECP·DEGF
(CEL) CE16965	238KNV·KVNVDIAFLIEMKEARRIDTMKIMELKVE·K·GP·LIGKLSGEAVELPDGRITQDPQWPSDDKVEGDKPLL·LWTECTTETH·
(ATH) gi6850339	203LSVTVCELPELCKEDLEKAKK·VFGVKPGPKYSRLQSGESVKS·DERDITVHPSDVMGP·SIPGPIVILVDCPTTSHA
(SCE) YKR079C	181VELPDLDAKVEVSTNYHISFSPVRGKFEVEAIKIGVE·K·GP·LFAKLTKGQTIHLDNGIWTPEQMLENER·HFAKMLILDIP·DDL
(HSA) ELAC2	317	IQPTICENATFORQGGADAPVAL·VHMMA PASVLVDSRQVQW·MERFEGPDTQ·HLVLNENCASVHNL·RSHKIQTQNLNHPDIFELL.....
(MMU) Elac2	313	IIPICENDFKRQVQATDAPVAL·AVHIAPESVLIDSRQVQW·MERFEGPDTQ·HLVLNENCASVHNL·RSHKIQTQNLNHPDIFELL.....
(CEL) CE16965	322	VKALIDSSSLQPFLENCKQLDY·VWHISDDAVINTPTVRL·MEKLNPPSITHLLINGNPNVPAVESVYVHTLIRSIAPSLFEAL.....
(ATH) gi6850339	280	AEHLSKLSLEYSSPDEQITGAKFVNCIHLSPSSVTSPTQSW·MKMFHL·TQ·HILAGQRFPLLIIVSHQAT·VKNMARPILKASSRIAA
(SCE) YKR079C	266	LMAFVEK·FKDYDCA·ELGWVYFLGDEVTINDNLPAFIDIFEKNNGKWNH·MISHNKISNTISFPGSALTITLKALQV·NNYNLPKTRDVFESKDF

FIG. 6A-1

FIG. 6A-2

(HSA) ELAC2	401	...TSFRCKKEGPTLSVNVQGECLKYQLRRREWQR.....DAITCNPEEFIVEAK.....QLPNFOOSVQEVRRSAQDG.
(MMU) Elac2	397	...TSFYSKEEGSTLSVTVRGECLKYQLRPKEWQR.....DTLDCNTDEFIARAL.....ELPSFQESVEEYRKNVQEN.
(CEL) CE16965	407	...HPIDWSGIITONEEISQRDQIRV·APNQRYWNR.....RGA·SPNEEPIVNNLLAAPELSDKAK·ELIKEYQK..
(ATH) gi6850339	374	RLNVCQOFFPAPGFWPQSLTDSNDPTPSNKF·NLRPVAIRGIDRSCIPAPLTSSEVDELLSIPKIDKSEBKQFNWKQHNTIIEKLWSECNT
(SCE) YKR079C	362	YDRPTPLSRGISMCKSQEPLNTHIEKDNHIFSQNKIVTFEPFRMNEEPKNCINGEVADFWSQBIFFEE·HVKPL·EPPLADVD·TVINNQLHVDN..
1641 insg		
(HSA) ELAC2	471	..PAPAEKRSQYPEIIF·LGTGSAIPMKIRNWSATLWNISP.....DTSLLDCCGCTFGQLCRHYGDQ·VDRNLGTLAAVFWSHLHADHHTGLPSI
(MMU) Elac2	467	..PAPAEKRSQYPEIIV·LGTGSAIPMEIRNWSSTLVNLSIP.....DKSVLLDCCGCTFGQLCRHYGQQ·IDRVLCSLTAVFWSHLHADHHTGLNLN
(CEL) CE16965	475	..LXENKMDCEFPKLTFFGTSSAVPSKYRNWTG·YLVEASE.....NSAILIDVCEGTGQMAVFGEDCKQLLVNLCVLITHAHQDMMNGLYTI
(ATH) gi6850339	473	VLPNCLEKIRRDDMEIVILGTGSSQPSKYRNWSAIFIDIFS.....RGSLLDCCGCTLGLRRRYGLDGADEAWRLRCIMWISHIHADHHTGLARI
(SCE) YKR079C	456	·FNNSAEKKKHVEIIT..LGTGSAIPSKYRNWVSTLWKVPFTDADGNTINRMILDAGENTLGTHERMESQLAVKSIQDLKMIYLSHLHADHHTGLISV
(HSA) ELAC1	1	MSNDVTF·LGTGAAVPSPTRGSAVWLRCF.....GECWLFDCGCGTQTQL.....MKSQKAGNITKIFITTHLHGDHFFGLPGL
(Es_c) elac	1	MKRDLELNLIF·LGTGAGVPTTRRNWTA·ILLNLOHPT.....QSGWLFDCGCGTQHQL.....LHTAFNPGKLDKIFISHLHGDHFFGLPGL
(Syn_sp) gi2500943	1	MEITP·LGTSSGVPTTRNRWSS·IALRLPQ.....RAEIMLFDCCGCTQHOF.....LRSEVKISQLTRIFITTHLHGDHFFGLMGL
(Me_t) gi2622965	1	MNEVTF·LGTSSAVPSKXNRWTS·IALRIP.....GEIFLFDCCGCTQROM.....ALAGISPKVTRIFITTHLHGDHFFGLPGL

FIG. 6A-2

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(HSA) ELAC2	559	LQORALASLGKPLHPLVWAPNQLKAWLQQVHNQCQEVUHHISWIPAKCLOEGAELSSPAVERLISLLRTC	
(MMU) Elac2	555	LQREHALASLGKPFQPLVWAPNQLKAWLQQVHNHCQEIHHVSMIPAKCLOGAEVSNITLERLISLLET	
(CEL) CE16965	565	IARKEAFESLGAPYRPLVWCNRNWLKPMKTVSICFENIBHLLLEIVDISRYPLTPPGSGGPPGKRPRLPSPHLPPSRDLQDM	
(ATH) gi6850339	564	LALRSKLLKGVTHEPVIWVGPRLKRFDAVQRLDNEFLDCRSTTATSWASLESAGEAEGSLTQGSFMQSVFRSDISMNSSVLLC	LK
(SCE) YKR079C	554	LNEWYKYNKDDTSTIYVWTPWQYHAFWNEMLVLENKEILKRIKIYISCEHFINDSFVRMOTQSVPLAEFNEILKENSQESNRKLELDRDSSYRDVD	
(HSA) ELAC1	75	LC·TISLQSGSMVSKQPIEIVGPPVGLRDFIWRTWELSHTELVFHYV·HELVPADQCPABELKEFAHVNRA	DS
(Es c) elac	83	L·CSRMSGIIPLTIVGPGGIREFVETAL	
(Syn sp) gi2500943	75	L·ASSGLAGSGGIEIVGPEGLDYLEACC	
(Me t) gi2622965	74	L·QSMGFRGEEPLDVGPPGHEHLEHCEM	
(HSA) ELAC2	633	DLEEFOTCLVRECKH·AFGCALVHT	SGWKWVYSGDTMP·CEAL
(MMU) Elac2	629	DLEEFOTCLVRECKH·AFGCALVHS	SGWKWVYSGDTMP·CEAL
(CEL) CE16965	650	SSSFDKXAKLDELKAVQVHTRMANGVVRV	AGKRIWFSGDTKP·CDLL
(ATH) gi6850339	657	NLKKVLSIGLNDLISFPVHECPQAYGVVKAER	VNSVGEQLGKWKWVYSGDSRP·CPET
(SCE) YKR079C	651	LIRQMYEDLSIEYFOTCRAIHCDW·AVNSITFR	MDENNEHNTFKVSVYSGDTMP·CEAL
(HSA) ELAC1	163	NSYLLFDDEQFV·VKAFLRERIPSFESVVEKKRPGKLNQKLDLGVPPGPAYGKLKNGISVVLNGVTISPQDVLKPKPIVGRKIQILGDCSG	VVGD
(Es c) elac	130	GEILDDGLRK·WTAYPLEHLECYGRIEEDDPGALNAQALKAAGVPPGPIFQELKAKTITLEDGRQINGADYLAAPVPGKALAFGDTGE	CDAA
(Syn sp) gi2500943	122	N·GLIYEDKDFQ·VHCGLLKHRIIPAYGVVRVEEKQRPGRFNVEQAEALGIPFGPIYQQLKQKTVTLEDGRIRRGDLCEPPEPGRKFNVCYCTDTVF	CEEA
(Me t) gi2622965	121	G·TVV·EDDYR·VTSAPASGVSFNLANVCFEKKKPR·FLREKAIALGLKPGPAGKLRHRCIPVRVG·RIIMPEVLGSPKGVKVCYSGDTMP·CEV	

FIG. 6B-1

FIG. 6B-2

(HSA) ELAC2	674	VRNGK	..DATLIIHEATLEEDGLEEEAVEKTHSTTSQAISVGMRMAEFIMLNHFSQRYAKWPLPSPNFSEKVGVAEDHM
(NMU) Elac2	670	VQNGK	..DATLIIHEATLEEDGLEEEAVEKTHSTTSQAISVGMRMAEFIMLNHFSQRYAKWPLPSPDFNEKVGIAEDHM
(CEL) CE16965	699	VEGCK	..DADVLVHSTFEDGHEVDMTPKPKKLAKISSLADANKRHSMTMGQAVDVGKRMNAKHIIIITHSARYPKWPVLPEYLDKENIGVAMDNL	
(ATH) gi6850339	717	VRASR	..DATLIIHEATFEDALIEEALAKNHSTTKKAIDVGSAAWYRIVLIITHSARYPKWPVLESHMHTCIAFDLM
(SCE) YKR079C	708	SLRIGY	..NSDLIIHEATLEENQLLEDAVKKKHCTINEAIGVSNKMMNAKLIIITHSARYPKWPVLNNIDVMAREFCFAPDSM
(HSA) ELAC1	261	GGVKLCFEADLI	..IHEATLDDAQMDXAKEHCHSDPQMAATHAKLCRKRLVIITHSARYPKWPVLREGQTDGIAELKKQAESVL
(Es c) elac	226	LDIAK	..GVDVWVHEATLDTMEAKANSRGHSSTRQAATLAREAGVGLIIITHSARYPKWPVLQHLLRECRSIFPATLIA
(Syn_sp) gi2500943	219	IALAQ	..EADLIVHEATFAHQDAQJAFDRLHSTSTMAAQVALLANVKKLIIITHSARYPKWPVLQLENLLAEQAIFPNTFLA
(Me t) gi2622965	215	IKLAE	..GAELIIHESSTLEAGSEDXAEHSGHSTAREAEVARSAGVIITHSARYPKWPVLEVILEARQVFPVMDVA
▼R781						
(HSA) ELAC2	751	KWCFGDFPTMPKLI	..IPPLKALFAGDIEEMERREKRLQVRAALLSRELAGGLEDGEPEQPKRAHTEEPQAKKVRQA	
(NMU) Elac2	747	KWCFGDFPTMPKLI	..IPPLKALFAGDIEEMERREKRLQVRAALLSRELAGGLEDGEPEQPKRAHTEEPQAKKVRQA	
(CEL) CE16965	794	RWRFDHLPLVSKLI	..PIFREVFVAFELFELTIKKEQRLVKDKELSEKRGQLKA		
(ATH) gi6850339	794	SINMADLHVLPKVL	..PVFKTLFRDEMVEDEDDDVAMDDLKERAL		
(SCE) YKR079C	789	INDYKIGEQQRI	..FELINKAFVBEKEEEEDVDVDESVDLEVLKHKHKN		
(HSA) ELAC1	344	DLQEVTLAEDFMVIS	..PIKK			
(Es c) elac	304	NDF..TVFNV				
(Syn_sp) gi2500943	300	RDF..LTWEIPRRTADPAIAMST	..QASPA			
(Me t) gi2622965	291	DDL..MTVEVKAYDSSPDS				

FIG. 6B-2

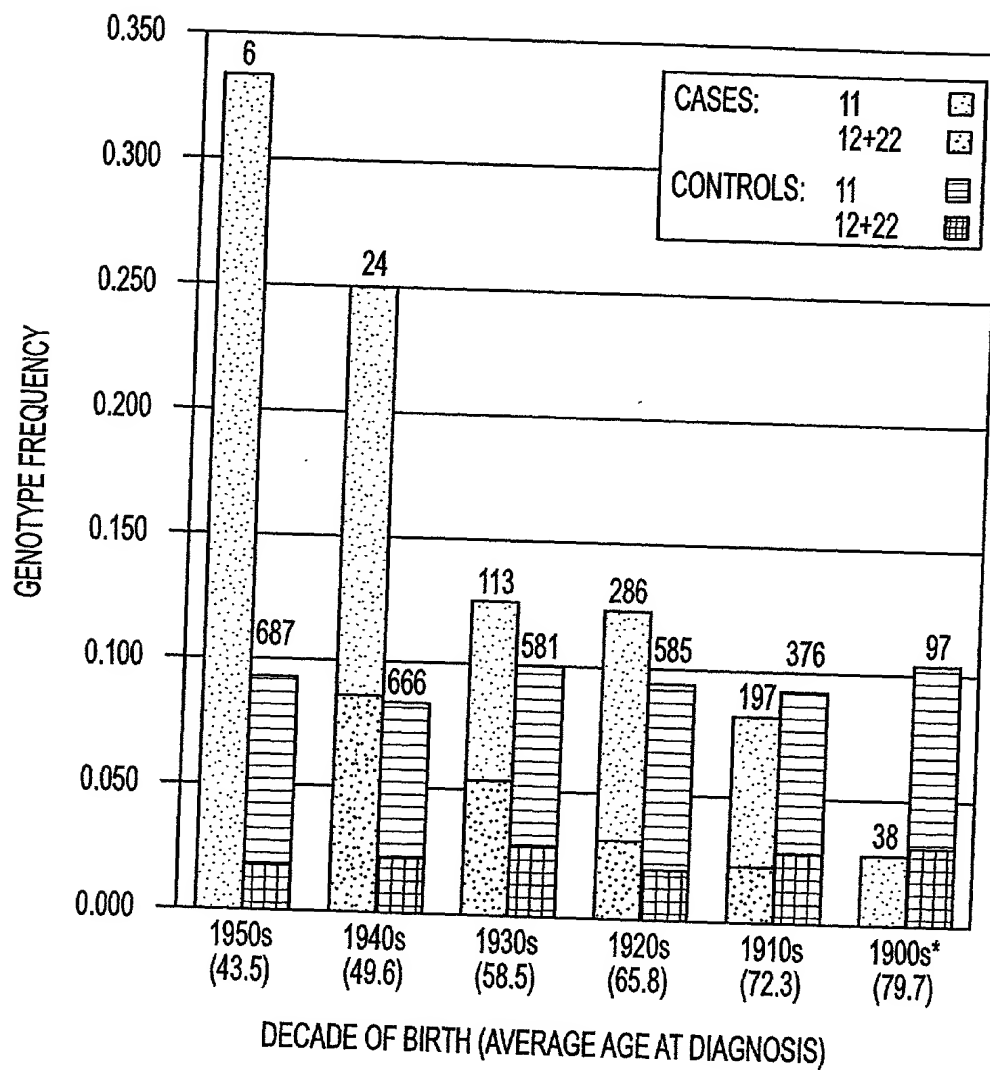


FIG. 7

FIG. 8

PS02 family

(HSA) ha3611	783	...GKQVLLDANHCPGAWMILFVLP.....NGTVILHTGDFRADPSPMERSLLADQX.....VHMLVLDITTYCSPEYTFPSQQQEVIRFAINTAF
(ATH) gi279557	484	...GIDVTCFDANHCPGSMILFEFA.....NGKAVHTGDFRISSEMSNWLGSH.....ISSLLIDITTYCNPQYDFPQAEAVIQFVVE·AI
(SCE) PS02	308	...TISVVTLDANHCPGALIMLFQEFPLA...NSYDKPIRQIHTGDFRBNAKMIETIQKWLAEATANEIDQVYLDITTYMNGYNGYFPSSQHSVCETVADFLL

FIG. 9-1

FIG. 9-2

FIG. 10

(HSA) ELAC2			(MMU) Elac2			(CEL) CE16965			(ATH) gi6850339			(SCE) YKR079C		
%ID	%SIM	%GAP	%ID	%SIM	%GAP	%ID	%SIM	%GAP	%ID	%SIM	%GAP	%ID	%SIM	%GAP
100.0	100.0	0.0	-	-	-	-	-	-	-	-	-	-	-	-
81.6	88.0	1.8	100.0	100.0	0.0	-	-	-	-	-	-	-	-	-
24.2	43.0	14.0	24.6	44.0	15.7	100.0	100.0	0.0	-	-	-	-	-	-
25.6	47.0	23.5	25.4	46.0	25.0	21.0	44.0	21.1	100.0	100.0	0.0	-	-	-
21.8	41.0	20.8	21.7	43.0	21.4	18.2	43.0	21.4	21.8	41.0	16.3	100.0	100.0	0.0

(HSA) ELAC2
 (MMU) Elac2
 (CEL) CE16965
 (ATH) gi6850339
 (SCE) YKR079C

FIG. 10

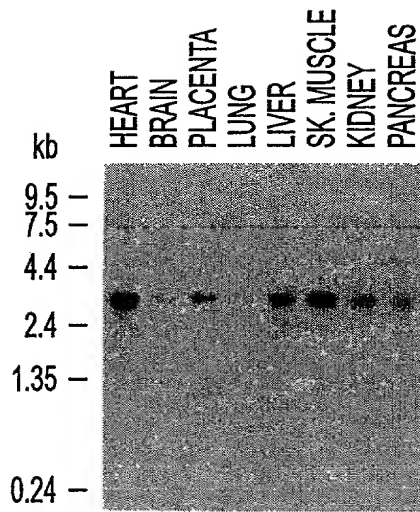


FIG. 11A

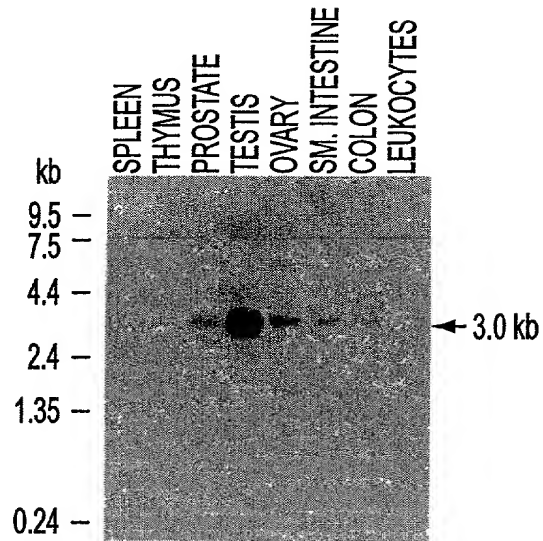


FIG. 11B



FIG. 11C



FIG. 11D

FIGURE 12

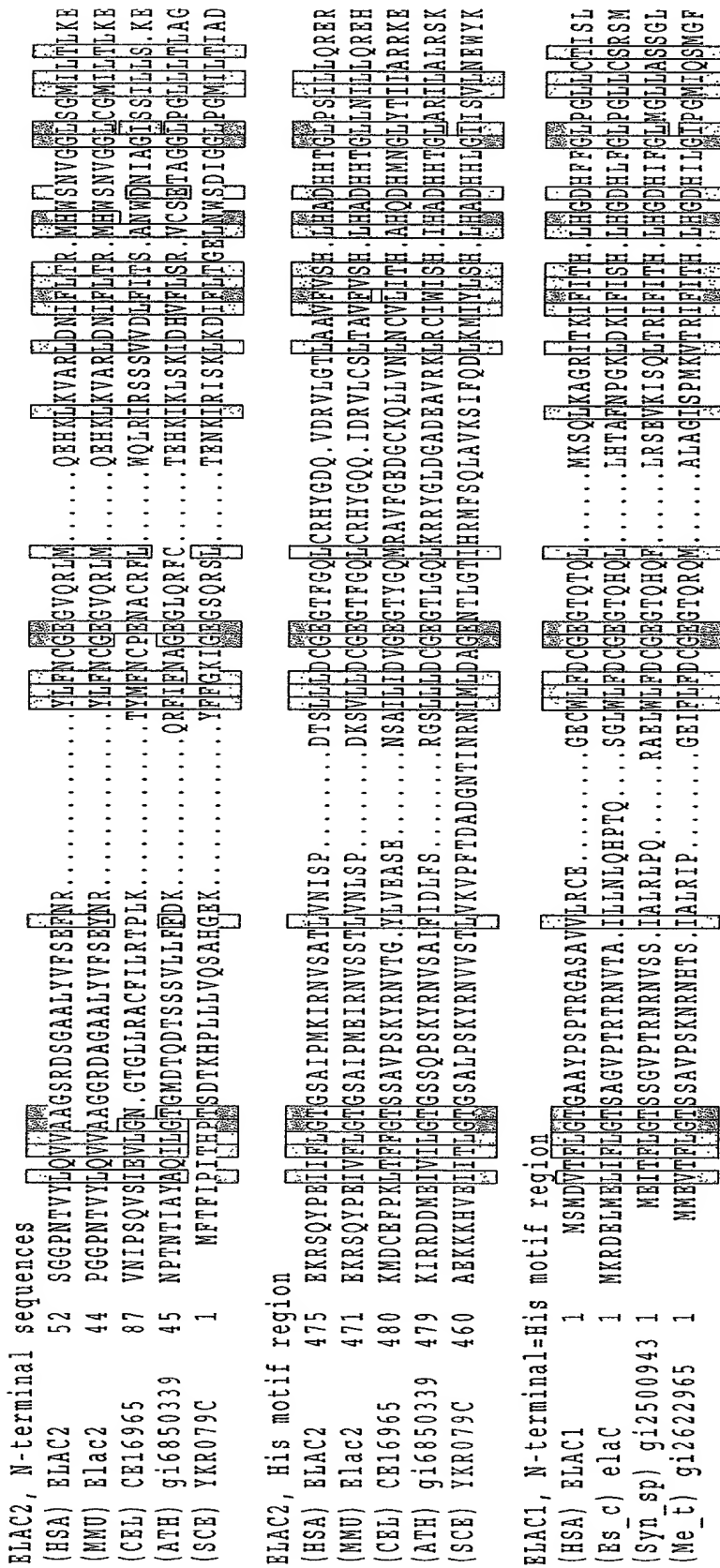


FIG. 12

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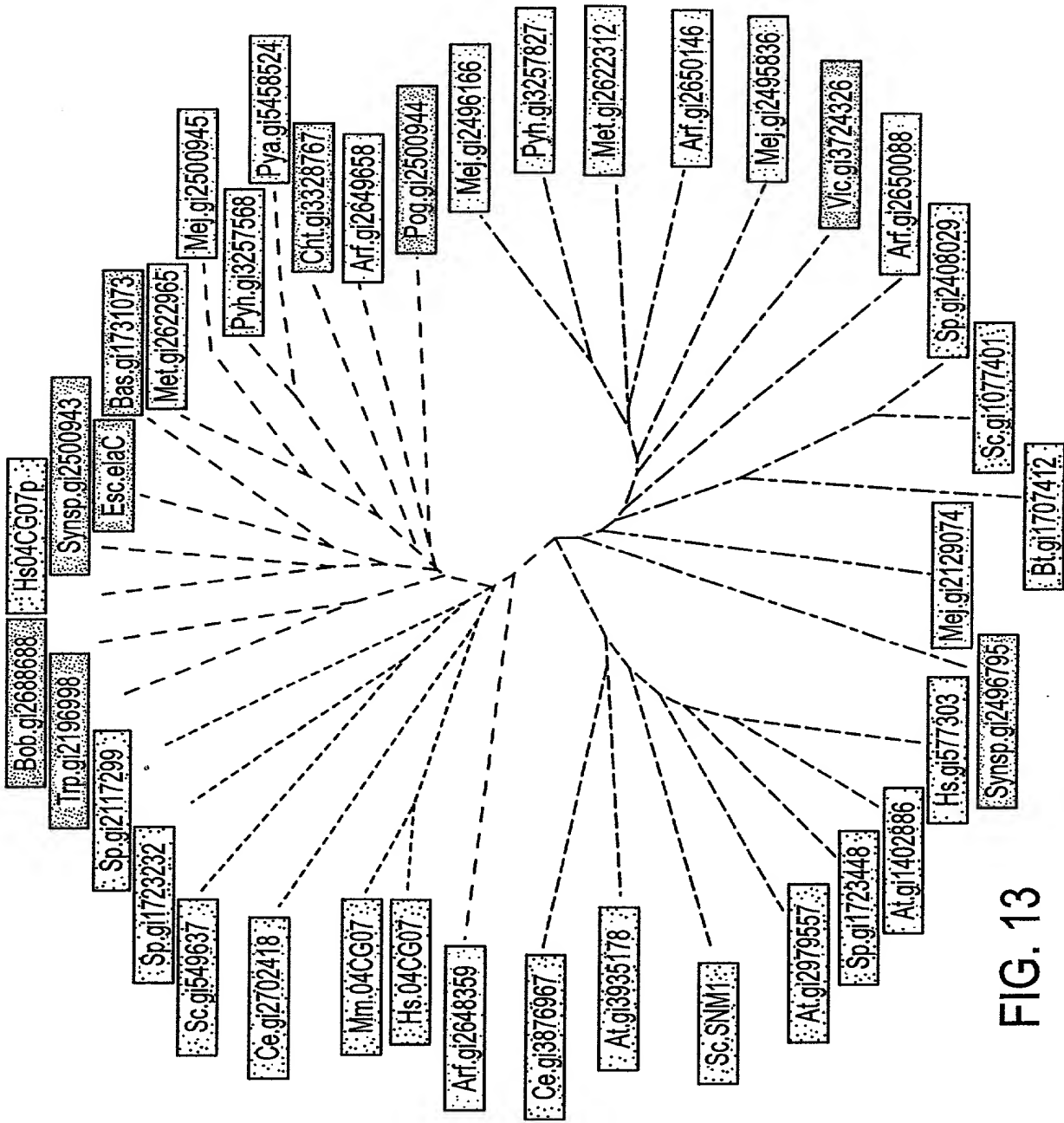
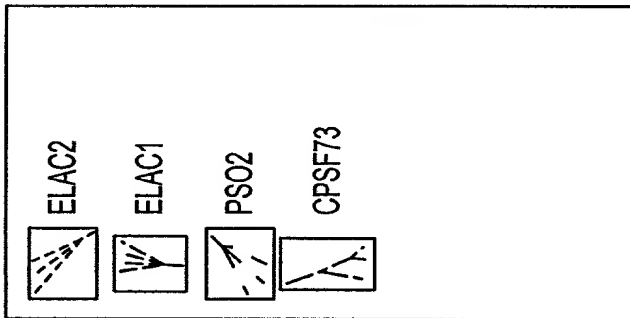


FIG. 13



Eukaryota
 Eubacteria
 Archaea